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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,419

DATE: 05/09/2002

TIME: 14:27:34

Input Set : A:\P2637-1(US).txt

Output Set: N:\CRF3\05092002\J020419.raw

3 <110> APPLICANT: Goddard,Audrey
4 Wood,William I.
5 Ye,Weilan
6 Zhang,Zemin
8 <120> TITLE OF INVENTION: NOVEL SECRETED POLYPEPTIDE AND METHODS OF TREATMENT OF
9 BONE DISORDERS
11 <130> FILE REFERENCE: P2637-1(US)
13 <140> CURRENT APPLICATION NUMBER: US 10/020,419
14 <141> CURRENT FILING DATE: 2001-12-13
16 <150> PRIOR APPLICATION NUMBER: US 60/132,379
17 <151> PRIOR FILING DATE: 1999-05-04
19 <150> PRIOR APPLICATION NUMBER: PCT/US00/05601
20 <151> PRIOR FILING DATE: 2000-03-01
22 <150> PRIOR APPLICATION NUMBER: PCT/US01/19692
23 <151> PRIOR FILING DATE: 2001-06-20
25 <150> PRIOR APPLICATION NUMBER: PCT/US01/21735
26 <151> PRIOR FILING DATE: 2001-07-09
28 <160> NUMBER OF SEQ ID NOS: 4
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 999
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo Sapien
35 <400> SEQUENCE: 1
36 gcgaggctgc accagcgctt ggcacccatga ggacgcctgg gcctctgccc 50
38 gtgctgctgc tgctcctggc gggagccccc gccgcgcggc ccactccccc 100
40 gacctgctac tcccgcctgc gggccctgag ccaggagatc acccgcgact 150
42 tcaacctcct gcagggtctcg gagccctcgg agccatgtgt gagatacctg 200
44 cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250
46 ggactttgtg gcctcgcccc cgtgttgga agtggccag gtagattcct 300
48 tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350
50 agagatttgg tattcctgtt ggatgactgc aatgccttgg aatacccaat 400
52 cccagtgcact acggctcctgc cagatcgtca gcgctaaggg aactgagacc 450
54 agagaaagaa cccaagagaa cttaaagttat gtcagctacc cagacttaat 500
56 gggccagagc catgaccctc acaggctctt tggttagttgt atctgaaact 550
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60 gaacctcctt tgagcataga gtttagcaacc atgcttctca ttcccttgac 650
62 tcatgtcttg ccaggatggt tagatacaca gcatgttgat ttggtcacta 700
64 aaaagaagaa aaggactaac aagcttcact tttatgaaca actattttga 750
66 gaacatgcac aatagtatgt ttttattact ggtttaatgg agtaatggtg 800
68 cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850
70 tatgcctttt tctaacacag acttttttca ctgtctttca tttaaaaaga 900
72 aattaatgct ctaagatat attttttacg tagtgctgac aggaccact 950
74 ctttcattga aagggtgatga aaatcaaata aagaatctct tcacatgga 999

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76 <210> SEQ ID NO: 2
77 <211> LENGTH: 136
78 <212> TYPE: PRT
79 <213> ORGANISM: Homo Sapien
81 <400> SEQUENCE: 2
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85 Gly Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg
86           20           25           30
88 Met Arg Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu
89           35           40           45
91 Gln Val Ser Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg
92           50           55           60
94 Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg
95           65           70           75
97 Asp Phe Val Ala Ser Pro Pro Cys Trp Lys Val Ala Gln Val Asp
98           80           85           90
100 Ser Leu Lys Asp Lys Ala Arg Lys Leu Tyr Thr Ile Met Asn Ser
101           95          100          105
103 Phe Cys Arg Arg Asp Leu Val Phe Leu Leu Asp Asp Cys Asn Ala
104          110          115          120
106 Leu Glu Tyr Pro Ile Pro Val Thr Thr Val Leu Pro Asp Arg Gln
107          125          130          135
109 Arg
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113 <211> LENGTH: 579
114 <212> TYPE: DNA
115 <213> ORGANISM: Homo Sapien
117 <400> SEQUENCE: 3
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120 tggcctctgg cagtacagtc cgcgcccccc acctgctact ctcgatgct 100
122 gaccctgagc cgtgagatca tggcagactt ccagagcctg caggcttcag 150
124 agcctgagga ttctgtgtg aggtacttgc cccggcttta cctggacatc 200
126 cataactact gtgtgctggc caagctgaga gacttcgtgg cttctcctca 250
128 gtgctggaag atggccgaag tggacactct gaaggacaga gtgcggaagc 300
130 tgtataccat catgaactcc ttctgcaggc gggacttggg attcctctca 350
132 gatgactgca gtgccttaga agaccaatt cccgaggcca cgggtcctcc 400
134 agactggcag agctaagcag gtggaccaga agaacaaccc agaggtctga 450
136 agctgggcca gttgtccaga gttacacccc ccacacacac acccaggtct 500
138 acttttagtg ccactgttag acctgccaca tgtctctagc ttctgaaaca 550
140 ccagtgaggg tcctacctct gagcatgct 579
142 <210> SEQ ID NO: 4
143 <211> LENGTH: 136
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo Sapien
147 <400> SEQUENCE: 4
148 Lys Thr Leu Pro Leu Leu Leu Leu Val Val Val Ile Ala
149   1           5           10           15
151 Trp Pro Leu Ala Val Gln Ser Ala Pro Pro Thr Cys Tyr Ser Arg

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152		20		25		30
154	Met Leu Thr Leu Ser Arg Glu Ile Met Ala Asp Phe Gln Ser Leu					
155		35		40		45
157	Gln Ala Ser Glu Pro Glu Asp Ser Cys Val Arg Tyr Leu Pro Arg					
158		50		55		60
160	Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Ala Lys Leu Arg					
161		65		70		75
163	Asp Phe Val Ala Ser Pro Gln Cys Trp Lys Met Ala Glu Val Asp					
164		80		85		90
166	Thr Leu Lys Asp Arg Val Arg Lys Leu Tyr Thr Ile Met Asn Ser					
167		95		100		105
169	Phe Cys Arg Arg Asp Leu Val Phe Leu Ser Asp Asp Cys Ser Ala					
170		110		115		120
172	Leu Glu Asp Pro Ile Pro Glu Ala Thr Gly Pro Pro Asp Trp Gln					
173		125		130		135
175	Ser					

VERIFICATION SUMMARY

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